



SEQUENCE LISTING

<110> Hitoshi, Yasumi
Demo, Susan
Jenkins, Yonchu
Rigel Pharmaceuticals, Inc.

<120> MRE11: Modulation of Cellular Proliferation

<130> 021044-001310US

<140> US 10/026,331

<141> 2001-12-21

<150> US 60/309,737

<151> 2001-08-01

<160> 21

<170> PatentIn Ver. 2.1

<210> 1

<211> 2537

<212> DNA

<213> Homo sapiens

<220>

<223> human MRE11 meiotic recombination 11 homolog A

<220>

<221> CDS

<222> (171)..(2297)

<223> MRE11

<400> 1

ccacgcgtcc	gggacgccgt	tctctcccgc	ggaattcagg	tttacggccc	tgcgggttct	60
cagagaattt	ctagaatttg	gaatcgagt	cattttctga	catttgagta	cagtaccag	120
gggttcttgg	agaagaacct	gggtcccag	gagcttgact	gaccataaaa	atgagtactg	180
cagatgcact	tgatgatgaa	aacacattta	aatattagt	tgcaacagat	attcatcttg	240
gatttatgga	gaaagatgca	gtcagaggaa	atgatacgtt	tgtaacactc	gatgaaattt	300
taagacttgc	ccaggaaaat	gaagtggatt	ttattttgtt	aggtgggtgat	ctttttcatg	360
aaaataagcc	ctcaaggaaa	acattacata	cctgcctcga	gttattaaga	aaatattgta	420
tgggtgatcg	gcctgtccag	tttgaaattc	tcagtgatca	gtcagtcaac	tttggtttta	480
gtaagtttcc	atgggtgaac	tatcaagatg	gcaacctcaa	catttcaatt	ccagtgttta	540
gtattcatgg	caatcatgac	gatcccacag	gggcagatgc	actttgtgcc	ttggacattt	600
taagtgtg	tggatttgta	aatcactttg	gacgttcaat	gtctgtggag	aagatagaca	660
ttagtccggt	tttgcttcaa	aaaggaagca	caaagattgc	gctatatggt	ttaggatcca	720
ttccagatga	aaggctctat	cgaatgtttg	tcaataaaaa	agtaacaatg	ttgagaccaa	780
aggaagatga	gaactcttgg	tttaacttat	ttgtgattca	tcagaacagg	agtaaacatg	840
gaagtactaa	cttcattcca	gaacaatttt	tggatgactt	cattgatctt	gttatctggg	900
gccatgaaca	tgagtgtaaa	atagctccaa	ccaaaaatga	acaacagctg	ttttatatct	960
cacaacctgg	aagctcagtg	gttacttctc	tttccccagg	agaagctgta	aagaaacatg	1020
ttggtttgct	gcgtattaaa	gggaggaaga	tgaatatgca	taaaattcct	cttcacacag	1080
tgcggcagtt	agtgaggag	gatattgttc	tagctaatac	tccagacatt	tttaaccagg	1140
ataatcctaa	agtaacccaa	gccatacaaa	gcttctgttt	ggagaagatt	gaagaaatgc	1200
ttgaaaatgc	tgaacgggaa	cgtctgggta	attctcacca	gccagagaag	cctctgttac	1260
gactgagagt	ggactatagt	ggagggtttg	aacctttcag	tggtcttcgc	tttagccaga	1320
aattttgtgga	tggggtagct	aatccaaaag	acattatcca	ttttttcagg	catagagAAC	1380
aaaaggaaaa	aacaggagaa	gagatcaact	ttgggaaact	tatcacaaag	ccttcagaag	1440
gaacaacttt	aagggtagaa	gatcttgtaa	aacagtactt	tcaaaccgca	gagaagaatg	1500
tgcagctctc	actgctaaca	gaaagaggga	tgggtgaagc	agtacaagaa	tttgtggaca	1560

RECEIVED
JUL 13 2002
COPY OF PAPERS
ORIGINALLY FILED
TECH CENTER 1600/2900

```

aggaggagaa agatgccatt gaggaattag tgaaatacca gttggaaaaa acacagcgat 1620
ttcttaaaga acgtcatatt gatgccctcg aagacaaaat cgaatgaggag gtacgtcggt 1680
tcagagaaac cagacaaaaa aataactaatg aagaagatga tgaagtccgt gaggtatga 1740
ccagggccag agcactcaga tctcagtcag aggagtctgc ttctgccttt agtgctgatg 1800
accttatgag tatagattta gcagaacaga tggctaataga ctctgatgat agcatctcag 1860
cagcaaccaa caaaggaaga ggccgaggaa gaggtcgaag aggtggaaga gggcagaatt 1920
cagcatcgag aggaggggtct caaagaggaa gagcagacac tggctctggag acttctaccc 1980
gtagcaggaa ctcaaagact gctgtgtcag catctagaaa tatgtctatt atagatgcct 2040
ttaaatctac aagacagcag ccttcccga atgtcactac taagaattat tcagagggtga 2100
ttgaggtaga tgaatcagat gtggaagaag acatttttcc taccacttca aagacagatc 2160
aaagggtggc cagcacatca tccagcaaaa tcatgtccca gagtcaagta tcgaaagggg 2220
ttgattttga atcaagttag gatgatgatg atgatccttt tatgaacact agttctttaa 2280
gaagaaatag aagataatat atttaatggc actgagaaac atgcaagata caggaaaaat 2340
gaaaatgtta caagctaaga gtttacagtt taagatttta agtattgttt cctgagcata 2400
actccataag taagaaattt ctagttcaca gacatacaat agcattgatt caccttggtt 2460
ttttaacctg gttgtgtgag taagagcttt gtttcaatat cactcttgag taaagattaa 2520
aataaagcta ccattttt                                     2537

```

```

<210> 2
<211> 708
<212> PRT
<213> Homo sapiens

```

```

<220>
<223> human MRE11 meiotic recombination 11 homolog A

```

```

<400> 2
Met Ser Thr Ala Asp Ala Leu Asp Asp Glu Asn Thr Phe Lys Ile Leu
 1          5          10          15
Val Ala Thr Asp Ile His Leu Gly Phe Met Glu Lys Asp Ala Val Arg
          20          25          30
Gly Asn Asp Thr Phe Val Thr Leu Asp Glu Ile Leu Arg Leu Ala Gln
          35          40          45
Glu Asn Glu Val Asp Phe Ile Leu Leu Gly Gly Asp Leu Phe His Glu
          50          55          60
Asn Lys Pro Ser Arg Lys Thr Leu His Thr Cys Leu Glu Leu Leu Arg
          65          70          75          80
Lys Tyr Cys Met Gly Asp Arg Pro Val Gln Phe Glu Ile Leu Ser Asp
          85          90          95
Gln Ser Val Asn Phe Gly Phe Ser Lys Phe Pro Trp Val Asn Tyr Gln
          100          105          110
Asp Gly Asn Leu Asn Ile Ser Ile Pro Val Phe Ser Ile His Gly Asn
          115          120          125
His Asp Asp Pro Thr Gly Ala Asp Ala Leu Cys Ala Leu Asp Ile Leu
          130          135          140
Ser Cys Ala Gly Phe Val Asn His Phe Gly Arg Ser Met Ser Val Glu
          145          150          155          160
Lys Ile Asp Ile Ser Pro Val Leu Leu Gln Lys Gly Ser Thr Lys Ile
          165          170          175
Ala Leu Tyr Gly Leu Gly Ser Ile Pro Asp Glu Arg Leu Tyr Arg Met
          180          185          190
Phe Val Asn Lys Lys Val Thr Met Leu Arg Pro Lys Glu Asp Glu Asn
          195          200          205
Ser Trp Phe Asn Leu Phe Val Ile His Gln Asn Arg Ser Lys His Gly
          210          215          220
Ser Thr Asn Phe Ile Pro Glu Gln Phe Leu Asp Asp Phe Ile Asp Leu
          225          230          235          240
Val Ile Trp Gly His Glu His Glu Cys Lys Ile Ala Pro Thr Lys Asn
          245          250          255

```

Glu	Gln	Gln	Leu	Phe	Tyr	Ile	Ser	Gln	Pro	Gly	Ser	Ser	Val	Val	Thr			
			260					265					270					
Ser	Leu	Ser	Pro	Gly	Glu	Ala	Val	Lys	Lys	His	Val	Gly	Leu	Leu	Arg			
		275					280					285						
Ile	Lys	Gly	Arg	Lys	Met	Asn	Met	His	Lys	Ile	Pro	Leu	His	Thr	Val			
		290				295					300							
Arg	Gln	Phe	Phe	Met	Glu	Asp	Ile	Val	Leu	Ala	Asn	His	Pro	Asp	Ile			
305					310					315					320			
Phe	Asn	Pro	Asp	Asn	Pro	Lys	Val	Thr	Gln	Ala	Ile	Gln	Ser	Phe	Cys			
				325					330					335				
Leu	Glu	Lys	Ile	Glu	Glu	Met	Leu	Glu	Asn	Ala	Glu	Arg	Glu	Arg	Leu			
			340					345					350					
Gly	Asn	Ser	His	Gln	Pro	Glu	Lys	Pro	Leu	Val	Arg	Leu	Arg	Val	Asp			
		355					360					365						
Tyr	Ser	Gly	Gly	Phe	Glu	Pro	Phe	Ser	Val	Leu	Arg	Phe	Ser	Gln	Lys			
		370				375					380							
Phe	Val	Asp	Arg	Val	Ala	Asn	Pro	Lys	Asp	Ile	Ile	His	Phe	Phe	Arg			
385					390					395					400			
His	Arg	Glu	Gln	Lys	Glu	Lys	Thr	Gly	Glu	Glu	Ile	Asn	Phe	Gly	Lys			
				405					410					415				
Leu	Ile	Thr	Lys	Pro	Ser	Glu	Gly	Thr	Thr	Leu	Arg	Val	Glu	Asp	Leu			
			420					425					430					
Val	Lys	Gln	Tyr	Phe	Gln	Thr	Ala	Glu	Lys	Asn	Val	Gln	Leu	Ser	Leu			
		435					440					445						
Leu	Thr	Glu	Arg	Gly	Met	Gly	Glu	Ala	Val	Gln	Glu	Phe	Val	Asp	Lys			
		450				455					460							
Glu	Glu	Lys	Asp	Ala	Ile	Glu	Glu	Leu	Val	Lys	Tyr	Gln	Leu	Glu	Lys			
465					470					475					480			
Thr	Gln	Arg	Phe	Leu	Lys	Glu	Arg	His	Ile	Asp	Ala	Leu	Glu	Asp	Lys			
				485					490					495				
Ile	Asp	Glu	Glu	Val	Arg	Arg	Phe	Arg	Glu	Thr	Arg	Gln	Lys	Asn	Thr			
			500					505					510					
Asn	Glu	Glu	Asp	Asp	Glu	Val	Arg	Glu	Ala	Met	Thr	Arg	Ala	Arg	Ala			
		515					520					525						
Leu	Arg	Ser	Gln	Ser	Glu	Glu	Ser	Ala	Ser	Ala	Phe	Ser	Ala	Asp	Asp			
		530				535					540							
Leu	Met	Ser	Ile	Asp	Leu	Ala	Glu	Gln	Met	Ala	Asn	Asp	Ser	Asp	Asp			
545					550					555					560			
Ser	Ile	Ser	Ala	Ala	Thr	Asn	Lys	Gly	Arg	Gly	Arg	Gly	Arg	Gly	Arg			
				565					570					575				
Arg	Gly	Gly	Arg	Gly	Gln	Asn	Ser	Ala	Ser	Arg	Gly	Gly	Ser	Gln	Arg			
			580					585					590					
Gly	Arg	Ala	Asp	Thr	Gly	Leu	Glu	Thr	Ser	Thr	Arg	Ser	Arg	Asn	Ser			
		595					600					605						
Lys	Thr	Ala	Val	Ser	Ala	Ser	Arg	Asn	Met	Ser	Ile	Ile	Asp	Ala	Phe			
		610				615					620							
Lys	Ser	Thr	Arg	Gln	Gln	Pro	Ser	Arg	Asn	Val	Thr	Thr	Lys	Asn	Tyr			
625					630					635					640			
Ser	Glu	Val	Ile	Glu	Val	Asp	Glu	Ser	Asp	Val	Glu	Glu	Asp	Ile	Phe			
				645					650					655				
Pro	Thr	Thr	Ser	Lys	Thr	Asp	Gln	Arg	Trp	Ser	Ser	Thr	Ser	Ser	Ser			
			660					665					670					
Lys	Ile	Met	Ser	Gln	Ser	Gln	Val	Ser	Lys	Gly	Val	Asp	Phe	Glu	Ser			
		675					680					685						
Ser	Glu	Asp	Asp	Asp	Asp	Asp	Pro	Phe	Met	Asn	Thr	Ser	Ser	Leu	Arg			
		690				695					700							
Arg	Asn	Arg	Arg															
705																		

<210> 3
 <211> 299
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human MRE11 amino acids 9-307

<400> 3
 Asp Glu Asn Thr Phe Lys Ile Leu Val Ala Thr Asp Ile His Leu Gly
 1 5 10 15
 Phe Met Glu Lys Asp Ala Ala Arg Gly Asn Asp Thr Phe Val Thr Leu
 20 25 30
 Asp Glu Ile Leu Arg Leu Ala Gln Glu Asn Glu Val Asp Phe Ile Leu
 35 40 45
 Leu Gly Gly Asp Leu Phe His Glu Asn Lys Pro Ser Arg Lys Thr Leu
 50 55 60
 His Thr Cys Leu Glu Leu Leu Arg Lys Tyr Cys Met Gly Asp Arg Pro
 65 70 75 80
 Val Gln Phe Glu Ile Leu Ser Asp Gln Ser Val Asn Phe Gly Phe Ser
 85 90 95
 Lys Phe Pro Trp Val Asn Tyr Gln Asp Gly Asn Leu Asn Ile Ser Ile
 100 105 110
 Pro Val Phe Ser Ile His Gly Asn His Asp Asp Pro Thr Gly Ala Asp
 115 120 125
 Ala Leu Cys Ala Leu Asp Ile Leu Ser Cys Ala Gly Phe Val Asn His
 130 135 140
 Phe Gly Arg Ser Met Ser Val Glu Lys Ile Asp Ile Ser Pro Val Leu
 145 150 155 160
 Leu Gln Lys Gly Ser Thr Lys Ile Ala Leu Tyr Gly Leu Gly Ser Ile
 165 170 175
 Pro Asp Glu Arg Leu Tyr Arg Met Phe Val Asn Lys Lys Val Thr Met
 180 185 190
 Leu Arg Pro Lys Glu Asp Glu Asn Ser Trp Phe Asn Leu Phe Val Ile
 195 200 205
 His Gln Asn Arg Ser Lys His Gly Ser Thr Asn Phe Ile Pro Glu Gln
 210 215 220
 Phe Leu Asp Asp Phe Ile Asp Leu Val Ile Trp Gly His Glu His Glu
 225 230 235 240
 Cys Lys Ile Ala Pro Thr Lys Asn Glu Gln Leu Phe Tyr Ile Ser
 245 250 255
 Gln Pro Gly Ser Ser Val Val Thr Ser Leu Ser Pro Gly Glu Ala Val
 260 265 270
 Lys Lys His Val Gly Leu Leu Arg Ile Lys Gly Arg Lys Met Asn Met
 275 280 285
 His Lys Ile Pro Leu His Thr Val Arg Gln Phe
 290 295

<210> 4
 <211> 300
 <212> PRT
 <213> Saccharomyces cerevisiae

<220>
 <223> yeast MRE11 amino acids 5-304

<400> 4
 Asp Pro Asp Thr Ile Arg Ile Leu Ile Thr Thr Asp Asn His Val Gly
 1 5 10 15

Tyr	Asn	Glu	Asn	Asp	Pro	Ile	Thr	Gly	Asp	Asp	Ser	Trp	Lys	Thr	Phe
			20					25					30		
His	Glu	Val	Met	Met	Leu	Ala	Lys	Asn	Asn	Val	Asp	Met	Val	Val	
		35					40				45				
Gln	Ser	Gly	Asp	Leu	Phe	His	Val	Asn	Lys	Pro	Ser	Lys	Lys	Ser	Leu
		50				55				60					
Tyr	Gln	Val	Leu	Lys	Thr	Leu	Arg	Leu	Cys	Cys	Met	Gly	Asp	Lys	Pro
		65			70					75					80
Cys	Glu	Leu	Glu	Leu	Leu	Ser	Asp	Pro	Ser	Gln	Val	Phe	His	Tyr	Asp
				85					90					95	
Glu	Phe	Thr	Asn	Val	Asn	Tyr	Glu	Asp	Pro	Asn	Phe	Asn	Ile	Ser	Ile
			100					105					110		
Pro	Val	Phe	Gly	Ile	Ser	Gly	Asn	His	Asp	Asp	Ala	Ser	Gly	Asp	Ser
		115					120					125			
Leu	Leu	Cys	Pro	Met	Asp	Ile	Leu	His	Ala	Thr	Gly	Leu	Ile	Asn	His
		130				135					140				
Phe	Gly	Lys	Val	Ile	Glu	Ser	Asp	Lys	Ile	Lys	Val	Val	Pro	Leu	Leu
		145			150					155					160
Phe	Gln	Lys	Gly	Ser	Thr	Lys	Leu	Ala	Leu	Tyr	Gly	Leu	Ala	Ala	Val
			165					170						175	
Arg	Asp	Glu	Arg	Leu	Phe	Arg	Thr	Phe	Lys	Asp	Gly	Gly	Val	Thr	Phe
		180						185					190		
Glu	Val	Pro	Thr	Met	Arg	Glu	Gly	Glu	Trp	Phe	Asn	Leu	Met	Cys	Val
		195					200					205			
His	Gln	Asn	His	Thr	Gly	His	Thr	Asn	Thr	Ala	Phe	Leu	Pro	Glu	Gln
		210				215					220				
Phe	Leu	Pro	Asp	Phe	Leu	Asp	Met	Val	Ile	Trp	Gly	His	Glu	His	Glu
		225			230					235					240
Cys	Ile	Pro	Asn	Leu	Val	His	Asn	Pro	Ile	Lys	Asn	Phe	Asp	Val	Leu
			245					250						255	
Gln	Pro	Gly	Ser	Ser	Val	Ala	Thr	Ser	Leu	Cys	Glu	Ala	Glu	Ala	Gln
		260						265					270		
Pro	Lys	Tyr	Val	Phe	Ile	Leu	Asp	Ile	Lys	Tyr	Gly	Glu	Ala	Pro	Lys
		275					280					285			
Met	Thr	Pro	Ile	Pro	Leu	Glu	Thr	Ile	Arg	Thr	Phe				
		290				295					300				

<210> 5
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:consensus MRE11 peptide

<400> 5
 Gly Asp Leu Phe His
 1 5

<210> 6
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:consensus MRE11 peptide

<220>
<221> MOD_RES
<222> (5)
<223> Xaa = Arg or Lys

<220>
<221> MOD_RES
<222> (7)
<223> Xaa = Thr or Ser

<220>
<221> MOD_RES
<222> (9)
<223> Xaa = His or Tyr

<400> 6
Asn Lys Pro Ser Xaa Lys Xaa Leu Xaa
1 5

<210> 7
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus MRE11
peptide

<220>
<221> MOD_RES
<222> (5)
<223> Xaa = Arg or Lys

<400> 7
Cys Met Gly Asp Xaa Pro
1 5

<210> 8
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus MRE11
peptide

<220>
<221> MOD_RES
<222> (2)
<223> Xaa = Ile or Leu

<400> 8
Glu Xaa Leu Ser Asp
1 5

<210> 9
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus MRE11
peptide

<400> 9
Val Asn Tyr Glx Asp
1 5

<210> 10
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus MRE11
peptide

<400> 10
Asn Ile Ser Ile Pro Val Phe
1 5

<210> 11
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus MRE11
peptide

<400> 11
Gly Asn His Asp Asp
1 5

<210> 12
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus MRE11
peptide

<220>
<221> MOD_RES
<222> (1)
<223> Xaa = Val or Ile

<220>
<221> MOD_RES
<222> (6)
<223> Xaa = Arg or Lys

<400> 12
Xaa Asn His Phe Gly Xaa
1 5

<210> 13
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus MRE11
peptide

<220>
<221> MOD_RES
<222> (7)
<223> Xaa = Ile or Leu

<400> 13
Gln Lys Gly Ser Thr Lys Xaa Ala Leu Tyr Gly Leu
1 5 10

<210> 14
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus MRE11
peptide

<220>
<221> MOD_RES
<222> (5)
<223> Xaa = Tyr or Phe

<400> 14
Asp Glu Arg Leu Xaa Arg
1 5

<210> 15
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus MRE11
peptide

<400> 15
Trp Phe Asn Leu
1

<210> 16
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus MRE11
peptide

<220>
<221> MOD_RES
<222> (2)
<223> Xaa = Ile or Leu

<400> 16
Phe Xaa Pro Glu Gln Phe Leu
1 5

<210> 17
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus MRE11
peptide

<220>
<221> MOD_RES
<222> (3)
<223> Xaa = Ile or Leu

<220>
<221> MOD_RES
<222> (5)
<223> Xaa = Leu or Met

<400> 17
Asp Phe Xaa Asp Xaa Val Ile Trp Gly His Glu His Glu Cys
1 5 10

<210> 18
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus MRE11
peptide

<400> 18
Gln Pro Gly Ser Ser Val
1 5

<210> 19
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide
duplex substrate for MRE11 plate-based assay

```

<220>
<221> modified_base
<222> (1)
<223> n = c modified by biotin

<220>
<221> modified_base
<222> (27)
<223> n = 5-bromo-2'-deoxyuridine

<220>
<221> modified_base
<222> (40)
<223> n = 5-bromo-2'-deoxyuridine

<400> 19
nagccagaca gtggagtact accacbngtg tggcccaggn c
41

<210> 20
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide
duplex substrate for MRE11 plate-based assay

<400> 20
gacctggggcc acacagtggg agtactccac tgtctggctg
40

<210> 21
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:poly Gly
flexible linker

<220>
<221> MOD_RES
<222> (6)..(200)
<223> Gly residues from position 6 to 200 may be present
or absent

<400> 21
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
1 5 10 15
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
20 25 30
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
35 40 45
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
50 55 60
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
65 70 75 80
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
85 90 95

```

Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly
			100					105						110		
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly
		115					120						125			
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly
	130						135						140			
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly
145					150					155						160
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly
				165					170						175	
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly
			180						185					190		
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly									
		195					200									